Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/518,072_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3: this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES) — Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) _128_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFWP

RAW SEQUENCE LISTING   DATE: 12/20/2005
PATENT APPLICATION: US/10/518,072   TIME: 10:31:35

Input Set : A:\263365US0XPCT.txt
Output Set: N:\CRF4\12202005\J518072.raw

```
 3 <110> APPLICANT: Weill, Mylene
 4         Fort, Philippe
 5         Raymond, Michel
 6         Pasteur, Nicole
 8 <120> TITLE OF INVENTION: NOVEL ACETYLCHOLINESTERASE GENE RESPONSIBLE FOR
 9         INSECTICIDE RESISTANCE AND APPLICATIONS THEREOF
11 <130> FILE REFERENCE: 263365US0XPCT
13 <140> CURRENT APPLICATION NUMBER: 10/518,072
14 <141> CURRENT FILING DATE: 2004-12-16
16 <150> PRIOR APPLICATION NUMBER: FR 02/07622
17 <151> PRIOR FILING DATE: 2002-06-20
19 <150> PRIOR APPLICATION NUMBER: FR 02/13799
20 <151> PRIOR FILING DATE: 2002-11-05
23 <160> NUMBER OF SEQ ID NOS: 129
25 <170> SOFTWARE: PatentIn version 2.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 524
29 <212> TYPE: PRT
30 <213> ORGANISM: Anopheles gambiae
32 <400> SEQUENCE: 1
33 Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg Gly Ile Thr
34  1               5                  10                  15
36 Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val Trp Leu Gly Ile Pro
37              20                  25                  30
39 Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe Arg His Pro Arg Pro
40          35                  40                  45
42 Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr Thr Pro Pro Asn Ser
43      50                  55                  60
45 Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr
46  65                  70                  75                  80
49 Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn
50                  85                  90                  95
52 Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
53              100                 105                 110
55 Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr
56          115                 120                 125
58 Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu
59      130                 135                 140
61 Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly Thr Pro Glu
62 145                 150                 155                 160
64 Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn Leu Ala Leu Arg Trp
65                  165                 170                 175
67 Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser Arg Val Thr
```

Does Not Comply
orrected Diskette Neede

```
68            180                    185                    190
70 Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu His Leu Leu
71            195                    200                    205
73 Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala Ile Leu Gln Ser Gly
74       210                    215                    220
76 Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu Ala Thr Leu
77 225                    230                    235                    240
79 Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys Pro His Glu Pro Ser
80                 245                    250                    255
82 Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly Lys Asp Pro His Val
83            260                    265                    270
85 Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu Phe Pro Phe
86            275                    280                    285
88 Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu Thr Pro Gln Arg Ser
89       290                    295                    300
91 Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile Leu Thr Gly Ser Asn
92 305                    310                    315                    320
94 Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr Leu Thr Glu Leu Leu
95            325                    330                    335
97 Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe Leu Gln Ala
98            340                    345                    350
100 Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg Gln Ala Ile
101           355                    360                    365
103 Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp Asn Pro Asn Ser Asn
104      370                    375                    380
106 Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe Thr Cys Asn
107 385                    390                    395                    400
109 Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn Asn Val Tyr
110                405                    410                    415
112 Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp Pro Arg Trp
113           420                    425                    430
115 Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe Gly Glu Pro
116           435                    440                    445
118 Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu Lys Asp Phe Ser Arg
119      450                    455                    460
121 Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly Asn Pro Asn
122 465                    470                    475                    480
124 Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp Pro Lys His Thr Ala
125           485                    490                    495
127 His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Ser Phe Val Gly
128           500                    505                    510
130 Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys
131      515                    520
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 1932
137 <212> TYPE: DNA
138 <213> ORGANISM: Anopheles gambiae
140 <220> FEATURE:
141 <221> NAME/KEY: CDS
```

RAW SEQUENCE LISTING   DATE: 12/20/2005
PATENT APPLICATION: US/10/518,072   TIME: 10:31:35

Input Set : A:\263365US0XPCT.txt
Output Set: N:\CRF4\12202005\J518072.raw

```
142 <222> LOCATION: (1)..(1932)
144 <400> SEQUENCE: 2
145 atg ttt gtg tgt tgt ttt ttc ttt ctc tct ctc tct ttc tgt ggt tcc   48
146 Met Phe Val Cys Cys Phe Phe Phe Leu Ser Leu Ser Phe Cys Gly Ser
147 1               5                   10                  15
149 aac att tca gac gca ttt ttt aca cca tat ata ggt cac ggt gag tcc   96
150 Asn Ile Ser Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser
151             20                  25                  30
153 gta cga att ata gat gcc gag ttg ggc acg ctc gag cat gtc cac agt   144
154 Val Arg Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser
155         35                  40                  45
157 gga gca acg ccg cgg cga cgc ggc ctg acg agg cgc gag tca aac tcg   192
158 Gly Ala Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser
159     50                  55                  60
161 gac gcg aac gac aac gat ccg ctg gtg gtc aac acg gat aag ggg cgc   240
162 Asp Ala Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg
163 65                  70                  75                  80
165 atc cgc ggc att acg gtc gat gcg ccc agc ggc aag aag gtg gac gtg   288
166 Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val
167             85                  90                  95
169 tgg ctc ggc att ccc tac gcc cag ccg ccg gtc ggg ccg cta cgg ttc   336
170 Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe
171             100                 105                 110
173 cgt cat ccg cgg ccg gcc gaa aag tgg acc ggc gtg ctg aac acg acc   384
174 Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr
175         115                 120                 125
177 aca ccg ccc aac agc tgc gtg cag atc gtg gac acc gtg ttc ggc gac   432
178 Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp
179     130                 135                 140
181 ttc ccg ggc gcg acc atg tgg aac ccg aac acg ccc ctg tcc gag gac   480
182 Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp
183 145             150                 155                 160
185 tgt ctg tac att aac gtg gtg gca ccg cga ccc cgg ccc aag aat gcg   528
186 Cys Leu Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala
187             165                 170                 175
189 gcc gtc atg ctg tgg atc ttc ggc ggc ggc ttc tac tcc ggc acc gcc   576
190 Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala
191             180                 185                 190
193 acc ctg gac gtg tac gac cac cgg gcg ctt gcg tcg gag gag aac gtg   624
194 Thr Leu Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val
195         195                 200                 205
197 atc gtg gtg tcg ctg cag tac cgc gtg gcc agt ctg ggc ttc ctg ttt   672
198 Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe
199     210                 215                 220
201 ctc ggc acc ccg gaa gcg ccg ggc aat gcg gga ctg ttc gat cag aac   720
202 Leu Gly Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn
203 225                 230                 235                 240
205 ctt gcg cta cgc tgg gtg cgg gac aac att cac cgg ttc ggt ggc gat   768
206 Leu Ala Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp
```

```
207                  245              250              255
209 ccg tcg cgt gtg aca ctg ttc ggc gag agt gcc ggt gcc gtc tcg gtg    816
210 Pro Ser Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val
211              260              265              270
213 tcg ctg cat ctg ctg tcc gcc ctt tcc cgc gat ctg ttc cag cgg gcc    864
215 Ser Leu His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala
216          275              280              285
218 atc ctg cag agc ggc tcg ccg acg gca ccg tgg gca ttg gta tcg cgc    912
219 Ile Leu Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg
220          290              295              300
222 gag gaa gcc aca cta aga gca ctg cgg ttg gcc gag gcg gtc ggc tgc    960
223 Glu Glu Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys
224 305              310              315              320
226 ccg cac gaa ccg agc aag ctg agc gat gcg gtc gag tgc ctg cgc ggc    1008
227 Pro His Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly
228              325              330              335
230 aag gac ccg cac gtg ctg gtc aac aac gag tgg ggc acg ctc ggc att    1056
231 Lys Asp Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile
232              340              345              350
234 tgc gag ttc ccg ttc gtg ccg gtg gtc gac ggt gcg ttc ctg gac gag    1104
235 Cys Glu Phe Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu
236          355              360              365
238 acg ccg cag cgt tcg ctc gcc agc ggg cgc ttc aag aag acg gag atc    1152
239 Thr Pro Gln Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile
240          370              375              380
242 ctc acc ggc agc aac acg gag gag ggc tac tac ttc atc atc tac tac    1200
243 Leu Thr Gly Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr
244 385              390              395              400
246 ctg acc gag ctg ctg cgc aag gag gag ggc gtg acc gtg acg cgc gag    1248
247 Leu Thr Glu Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu
248          405              410              415
250 gag ttc ctg cag gcg gtg cgc gag ctc aac ccg tac gtg aac ggg gcg    1296
251 Glu Phe Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala
252          420              425              430
254 gcc cgg cag gcg atc gtg ttc gag tac acc gac tgg acc gag ccg gac    1344
255 Ala Arg Gln Ala Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp
256          435              440              445
258 aac ccg aac agc aac cgg gac gcg ctg gac aag atg gtg ggc gac tat    1392
259 Asn Pro Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr
260 450              455              460
262 cac ttc acc tgc aac gtg aac gag ttc gcg cag cgg tac gcc gag gag    1440
263 His Phe Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu
264 465              470              475              480
266 ggc aac aac gtc tac atg tat ctg tac acg cac cgc agc aaa ggc aac    1488
267 Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn
268              485              490              495
270 ccg tgg ccg cgc tgg acg ggc gtg atg cac ggc gac gag atc aac tac    1536
271 Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr
272              500              505              510
```

RAW SEQUENCE LISTING   DATE: 12/20/2005
PATENT APPLICATION: US/10/518,072   TIME: 10:31:35

Input Set : A:\263365US0XPCT.txt
Output Set: N:\CRF4\12202005\J518072.raw

```
274 gtg ttc ggc gaa ccg ctc aac ccc acc ctc ggc tac acc gag gac gag      1584
275 Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu
276         515                 520                 525
278 aaa gac ttt agc cgg aag atc atg cga tac tgg tcc aac ttt gcc aaa      1632
279 Lys Asp Phe Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys
280     530                 535                 540
282 acc ggg aat cca aat ccc aac acg gcc agc agc gaa ttc ccc gag tgg      1680
283 Thr Gly Asn Pro Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp
284 545                 550                 555                 560
286 ccc aag cac acc gcc cac gga cgg cac tat ctg gag ctg ggc ctc aac      1728
287 Pro Lys His Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn
288                 565                 570                 575
291 acg tcc ttc gtc ggt cgg ggc cca cgg ttg agg cag tgt gcc ttc tgg      1776
292 Thr Ser Phe Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp
293   .             580                 585                 590
295 aag aag tac ctt ccc cag cta gtt gca gct acc tcg aac cta cca ggg      1824
296 Lys Lys Tyr Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly
297         595                 600                 605
299 cca gca ccg cct agt gaa ccg tgc gaa agc agc gca ttt ttt tac cga      1872
300 Pro Ala Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg
301     610                 615                 620
303 cct gat ctg atc gtg ctg ctg gtg tcg ctg ctt acg gcg acc gtc aga      1920
304 Pro Asp Leu Ile Val Leu Leu Val Ser Leu Leu Thr Ala Thr Val Arg
305 625                 630                 635                 640
307 ttc ata caa taa                                                      1932
308 Phe Ile Gln
311 <210> SEQ ID NO: 3
312 <211> LENGTH: 643
313 <212> TYPE: PRT
314 <213> ORGANISM: Anopheles gambiae
316 <400> SEQUENCE: 3
317 Met Phe Val Cys Cys Phe Phe Phe Leu Ser Leu Ser Phe Cys Gly Ser
318  1               5                  10                  15
320 Asn Ile Ser Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser
321           .     20                 25                  30
323 Val Arg Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser
324         35                 40                  45
326 Gly Ala Thr Pro Arg Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser
327     50                 55                  60
329 Asp Ala Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg
330 65                 70                  75                  80
332 Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val
333                 85                 90                  95
335 Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe
336                 100                105                 110
338 Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr
339             115                120                 125
341 Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp
342     130                135                140
```

10/518,072   6

```
<210> SEQ ID NO 128
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: n=a,c,g, or t
<400> SEQUENCE: 128
      ccgggngcsa cyatgtggaa                                    20
```

needs explanation – see item 11 on Err Summary sheet (handwritten annotation)

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/20/2005
PATENT APPLICATION: US/10/518,072   TIME: 10:31:36

Input Set : **A:\263365US0XPCT.txt**
Output Set: **N:\CRF4\12202005\J518072.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the
<220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:128; N Pos. 6

<u>Invalid <213> Response:</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:39,40,41,42,43,44,45,46,47,48,49,50,54,55,58,59,123,124,128,129

VERIFICATION SUMMARY   DATE: 12/20/2005
PATENT APPLICATION: US/10/518,072   TIME: 10:31:36

Input Set : A:\263365US0XPCT.txt
Output Set: N:\CRF4\12202005\J518072.raw

L:6024 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128 after pos.:0